

SEQUENCE LISTING

<110> Johnson et al.

<120> INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
PATHWAY AND PRESENTATION TO CD4+ CELLS

<130> 0899-54203 Johnson

<140>

<141>

<150> 60/118,287

<151> 1999-02-02

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 600

<212> DNA

<213> Cytomegalovirus

<400> 1

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cgtgtatgac ttccgcacca tcccgtaactg catgttccac atgtacgcgc tagacgtgta 180
atccactcgc agttcgggga cgcaacgcag ccagatcaca tccccttgca gtaccagacg 240
cagggctagc gtctcgaaga tcggcatcac atctaagttc cgcacgttcc actttaacga 300
ctccccggga acgaactcca cgctcgtcggc gtgtacgtac aggttctctc ccacgccgcc 360
ataatcggcc ttcggatcga agacgaaccg actcatgttg cccacgatgc tcccccgagc 420
aaacaacttg ccgttgtcaa tgtagcaccg gttgtcctcg atttgaaacc agggatgctt 480
ggccgtggac ttccagggcc ggagcgcgctc ttccccgggt ttagtgattc catcgggcag 540
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<210> 2

<211> 600

<212> DNA

<213> Cytomegalovirus

<220>

<221> CDS

<222> (1)..(600)

<400> 2

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  1             5             10             15

ccc ttg atc cgc ctg ccc gat gga atc act aaa gcc ggg gaa gac gcg 96
Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
      20             25             30

ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa atc gag 144
Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu
      35             40             45

gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg ggg agc 192

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Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser
 50 55 60
 atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc gat tat 240
 Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr
 65 70 75 80
 ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg gag ttc 288
 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe
 85 90 95
 gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat gtg atg 336
 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met
 100 105 110
 ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg gat gtg 384
 Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val
 115 120 125
 atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg tct agc 432
 Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser
 130 135 140
 gcg tac atg tgg aac atg cag tac ggg atg gtg cgg aag tca tac acg 480
 Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr
 145 150 155 160
 cat gtg gcc tgg aca ata gtg ttt tac tcc ata aac att acc ctg ttg 528
 His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu
 165 170 175
 gta ttg ttt atc gtg tat gtg act gtg gac tgt aac ttg tct atg atg 576
 Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met
 180 185 190
 tgg atg cgg ttt ttc gtg tgc tga 600
 Trp Met Arg Phe Phe Val Cys
 195 200

<210> 3
 <211> 199
 <212> PRT
 <213> Cytomegalovirus

<400> 3
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 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu
 35 40 45
 Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser
 50 55 60
 Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr
 65 70 75 80
 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe
 85 90 95
 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met
 100 105 110

Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val
 115 120 125
 Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser
 130 135 140
 Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr
 145 150 155 160
 His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu
 165 170 175
 Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met
 180 185 190
 Trp Met Arg Phe Phe Val Cys
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<210> 4

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chimera

<220>

<221> CDS

<222> (1)..(534)

<400> 4

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tct tac atc tat gcg cgc ctg ccc gat gga atc act aaa gcc ggg gaa 96
 Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
 20 25 30

gac gcg ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa 144
 Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
 35 40 45

atc gag gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg 192
 Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
 50 55 60

ggg agc atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc 240
 Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
 65 70 75 80

gat tat ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg 288
 Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
 85 90 95

gag ttc gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat 336
 Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
 100 105 110

gtg atg ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg 384
 Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
 115 120 125

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gat gtg atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg 432
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr
130 135 140

tct agc gcg tac atg tgg aac atg cag tac ggg atg gtg ggg cag cca 480
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro
145 150 155 160

gaa ctc gcc ccg gaa gac ccc gag gat tgc gcc ctc ttg gag gac ccc 528
Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
165 170 175

gtg tga 534
Val

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<210> 5
 <211> 177
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: chimera

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<400> 5
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Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
20 25 30
Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
35 40 45
Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
50 55 60
Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
65 70 75 80
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
85 90 95
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
100 105 110
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
115 120 125
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr
130 135 140
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro
145 150 155 160
Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
165 170 175
Val

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<210> 6
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Oligonucleotide
 <400> 6
 cgcgcatcca tgaacaatct ctggaaagcc tgg

33

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 7
cgtgaattcg acatgacaca cgtaatgggt act

33

09890806 111501

SEQUENCE LISTING

<110> Johnson et al.

<120> INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
 PATHWAY AND PRESENTATION TO CD4+ CELLS

<130> 0899-59399

<140>

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<150> US00/02740

<151> 2000-02-02

<150> 60/118,287

<151> 1999-02-02

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 600

<212> DNA

<213> Cytomegalovirus

<400> 1

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tcagcacacg aaaaaccgca tccacatcat agacaagtta cagtccacag tcacatacac 60
gataaacaat accaacaggg taatgtttat ggagtaaaac actattgtcc aggccacatg 120
cgtgtatgac ttccgcacca tcccgtaactg catgttccac atgtacgcgc tagacgtgta 180
atccactcgc agttcgggga cgcaacgcag ccagatcaca tccccttgca gtaccagacg 240
cagggctagc gtctcgaaga tcggcatcac atctaagttc cgcacgttcc actttaacga 300
ctccccggga acgaactcca cgtcgtcggc gtgtacgtac aggttctctc ccacgccgcc 360
ataatcggcc ttccgatcga agacgaaccg actcatgttg cccacgatgc tcccccgagc 420
aaacaacttg ccgttggtcaa tgtagcaccg gttgtcctcg atttgaaacc agggatgctt 480
ggccgtggac ttccagggcc ggagcgcgctc ttccccggct ttagtgattc catcgggcag 540
gcggatcaag ggaccatagg aggtccaaag acccaccacg gctttccaga gattgttcat 600
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<210> 2

<211> 600

<212> DNA

<213> cytomegalovirus

<220>

<221> CDS

<222> (1)..(600)

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ccc ttg atc cgc ctg ccc gat gga atc act aaa gcc ggg gaa gac gcg 96
Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
      20             25             30
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ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa atc gag	144
Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu	
35 40 45	
gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg ggg agc	192
Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser	
50 55 60	
atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc gat tat	240
Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr	
65 70 75 80	
ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg gag ttc	288
Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe	
85 90 95	
gtt ccc ggg gag tgc tta aag tgg aac gtg cgg aac tta gat gtg atg	336
Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met	
100 105 110	
ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg gat gtg	384
Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val	
115 120 125	
atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg tct agc	432
Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser	
130 135 140	
gcg tac atg tgg aac atg cag tac ggg atg gtg cgg aag tca tac acg	480
Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr	
145 150 155 160	
cat gtg gcc tgg aca ata gtg ttt tac tcc ata aac att acc ctg ttg	528
His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu	
165 170 175	
gta ttg ttt atc gtg tat gtg act gtg gac tgt aac ttg tct atg atg	576
Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met	
180 185 190	
tgg atg cgg ttt ttc gtg tgc tga	600
Trp Met Arg Phe Phe Val Cys	
195 199	

<210> 3
 <211> 199
 <212> PRT
 <213> cytomegalovirus

<400> 3
 Met Asn Asn Leu Trp Lys Ala Trp Val Gly Leu Trp Thr Ser Met Gly
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 Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
 20 25 30
 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu

gat tat ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg	288
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val	
85 90 95	
gag ttc gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat	336
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp	
100 105 110	
gtg atg ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg	384
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly	
115 120 125	
gat gtg atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg	432
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr	
130 135 140	
tct agc gcg tac atg tgg aac atg cag tac ggg atg gtg ggg cag cca	480
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro	
145 150 155 160	
gaa ctc gcc ccg gaa gac ccc gag gat tcg gcc ctc ttg gag gac ccc	528
Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro	
165 170 175	
gtg tga	534
Val	

<210> 5

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera

<400> 5

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile	
1 5 10 15	
Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu	
20 25 30	
Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln	
35 40 45	
Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg	
50 55 60	
Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala	
65 70 75 80	
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val	
85 90 95	
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp	
100 105 110	
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly	
115 120 125	
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr	
130 135 140	
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro	
145 150 155 160	

Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
165 170 175
Val

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 6
cgcggatcca tgaacaatct ctggaaagcc tgg 33

<210> 7
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

<400> 7
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